# Cyanogen Bromide (CNBr) Cleavage

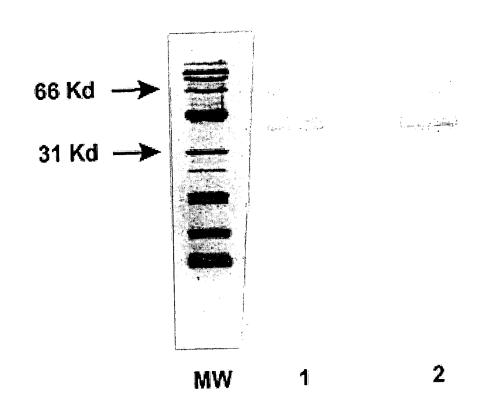
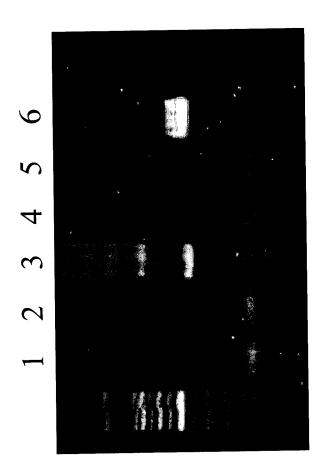


Figure 1

V



500 bases

**m** 

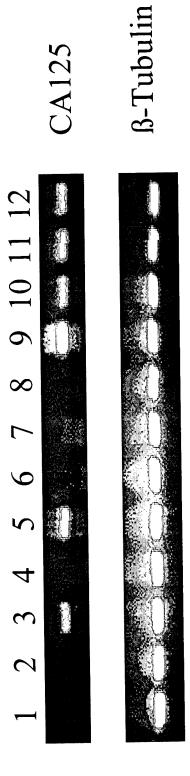
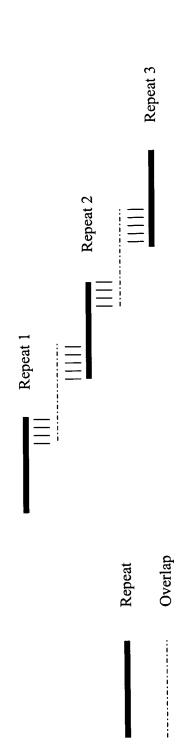


Figure 2

# 

# A Strategy for Placing Repeat Sequences in Contiguous Order Using Overlap Sequence Allignment



157 AAGPILMPFTINFTITNLQYEEDMRRTGSRKFNTMESVLQGLLKPLFKNTSVGPLYSGCRLTLLRPEKDGAATGVDAICTHRLDPKSPGLNREQLYWELSKLTNDIEELGPYTLDRNSLYVNGFTHQSSVSTTSTPGTSTVDLRTSGTPSSLSSPTIM 315 AAGPLIVPFTLNFTITNLQYGEDMGHPGSRKFNTTERVLQGLLGPIFKNTSVGPLYSGCRLTSLRSEKDGAATGVDAICIHHLDPKSPGLANRERLYWELSQLTNGIKELGPYTLDRNSLYVNGFTHRTSVPTSSTPGTSTVDLGTSGTPFSLPSPA 1 ATVPFMVPFTLNFTITNLQYEEDMRHPGSRKFNATERELQGLLKPLFRNSSLEYLYSGCRLASLRPEKDSSAMAVDAICTHRPDPEDLGLDRERLYWELSNLTNGIQELGPYTLDRNSLYVNGFTHRSSMPTTSTPGTSTVDVGTSGTPSSSPSPT

156 314 470

> 411 TAGPLLVLFTLNFTITNLKYEEDMHRPGSRKFNTTERVLQTLLGPMFKNTSVGLLYSGCRLTLLRSEKDGAATGVDAICTHRLDPKSPGLDREQLYWELSQLTNGIKELGPYTLDRNSLYVNGFTHWIPVPTSSTPGTSTVDLG.SGTPSSLPSPT 626 AAGPLLVPFTINFTITNLQYEEDMHHPGSRKFNTTERVLQGLLGPMFKNTSVGLLYSGCRLTLLRSEKDGAATGVDALCTHRLDPKSPGVDREQLYWELSQLTNGIKELGPYTLDRNSLYVNGFTHQTSAPNTSTPGTSTVDLGTSGTPSSLPSPT

625 EPGPLLIPFTFNFTITNLHYBENMQHPGSRKFNTTERVLQGLLKPLFRNTSVGPLYSGCRLTLLRPEKHEAATGVDTICTHRVDPIGPGLDRERLYWELSQLTNSITELGPYTLDRDSLYVNGFNPRSSVPTTSTPGTSTVHLATSGTPSSLPGHT 1 SAGPLLVPFTLNFTITNLQYEEDMHHPGSRKFNTTERVLQGLLGPMFKNTSVGLLYSGCRLTLLRPEKNGAATGMDAICSHRLDPKSPGLNREQLYWELSQLTHGIKELGPYTLDRNSLYVNGFTHRSSVAPTSTPGTSTVDLGTSGTPSSLPSPT 157 TAVPLLVPFTLNFTITNLQYGEDMRHPGSRKFNTTERVLQGLLGPLFKNSSVGPLYSGCRLISLRSEKDGAATGVDAICTHHLNPQSPGLDREQLYWQLSQMTNGIKELGPYTLDRNSLYVNGFTHRSSGLTTSTPWTSTVDLGTSGTPSPVPSPT 313 TAGPLLVPFTLNFTITNLQYEEDMHRPGSRKFNATERVLQGLLSPIFKNSSVGPLYSGCRLTSLRPEKDGAATGMDAVCLYHPNPKRPGLDREQLYWELSQLTHNITELGPYSLDRDSLYVNGFTHQNSVPTTSTPGTSTVYWATTGTPSSFPGHT 469 EPGPLLIPFTENFTITNLHYEENMQHPGSRKFNTTERVLQGLLKPLFKNTSVGPLYSGCRLTSLRPEKDGATGMDAVCLYHPNPKRPGLDREQLYCELSQLTHNITELGPYSLDRDSLYVNGFTHQNSVPTTSTPGTSTVXWATTGTPSSFPGHT

62**4** 780

156 312 468 624

(SEQ ID NO: 160)

TAGPLLVPFTLNFTITNLQYEEDMHRPGSRRFNTTERVLQGLLTPLFKNTSVGPLYSGCRLTLLRPEKQEAATGVDTICTHRVDPIGPGLDRERLYWELSQLTNSITELGPYTLDRDSLYVNGFNPWSSVPTTSTPGTSTVHLATSGTPSSLPGHT 157 APVPLLIPFTINFTITDLHYEENMQHPGSRKFNTTERVLQGLLKPLFKSTSVGPLYSGCRLTLLRPEKHGAATGVDAICTLRLDPTGPGLDRERLYWELSQLTNSVTELGPYTLDRDSLYVNGFTHRSSVPTTSIPGTSAVHLETSGTPASLPGHT APGPILUPFTLNFTITNLQYEEDMRHPGSRKFSTTERVLQGLLKPLFKNTSVSSLYSGCRLTLLRPEKDGAATRVDAVCTHRPDPKSPGLDRERLYWKLSQLTHGITELGPYTLDRHSLYVNGFTHQSSMTTTRTPDTSTMHLATSRTPASLSGPT 469 TASPLLVLFTINFTITNQRYEENMHHPGSRKFNTTERVLQGLLRPVFKNTSVGPLYSGCRLTLLRPKKDGAATKVDAICTYRPDPKSPGLDREQLYWELSQLTHSITELGPYTQDRDSLYVNGFTHRSSVPTTSIPGTSAVHLETSGTPASLPCHT

313 AASPILVLFTLNGTITNLRYBENMQHPGSRKFNTTERVLQGLLRSLFKSTSVGPLYSGCRLTLLRPEKDGTATGVDALCTHHPDPKSPRLDREQLYWELSQLTHNITELGHYALDNDSLFVNGFTHRSSVSTTSTPGTPTVYLGASKTPASIFGPS 1 ATGPVILPFTINFTITNLQYEEDMHRPGSRKENTTERVLQGLLMPLFKNTSVSSLYSGCRLTLLRPEKDGAATRVDAVCTHRPDPKSPGLDRERLYWKLSQLTHGITELGPYTLDRHSLYVNGFTHQSSMTTTRTPDTSTMHLATSRTPASLSGPT 157 TASPLLVLFTINFTITNLRYEENMHHPGSRKFNTTERVLQGLLRPVFKNTSVGPLYSGCRLTLLRPKKDGAATKVDAICTYRPDPKSPGLDREQLYWELSQLTHSITELGPYTQDRDSLYNVGFTQRSSVPTTSVPGTPTVDLGTSGTPVSKPGPS

156 312 468

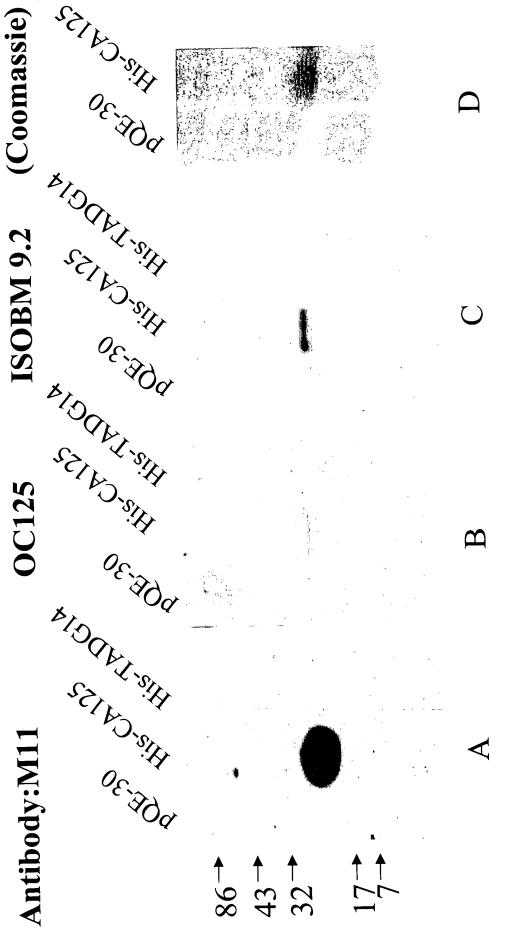
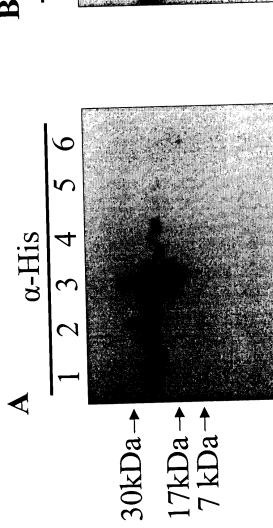
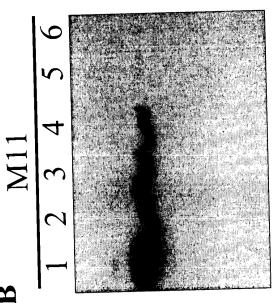


Figure 4





C- - - - C - - DRERLYWELS 0 0 00 QLTNSITELG PYTLDRDSLY VNGFNPRSSV PTTSTPGTST VHLATSGTPS EPGPLLIPFT FNFTITNLHY EENMQHPGSR KFNTTERVLQ GLLKPLFKNT 0 0000 00 SLPKLT 151 101 51

Figure 5 (SEQ ID NO: 150)

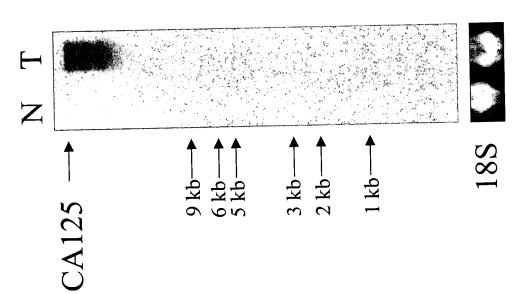


Figure 6

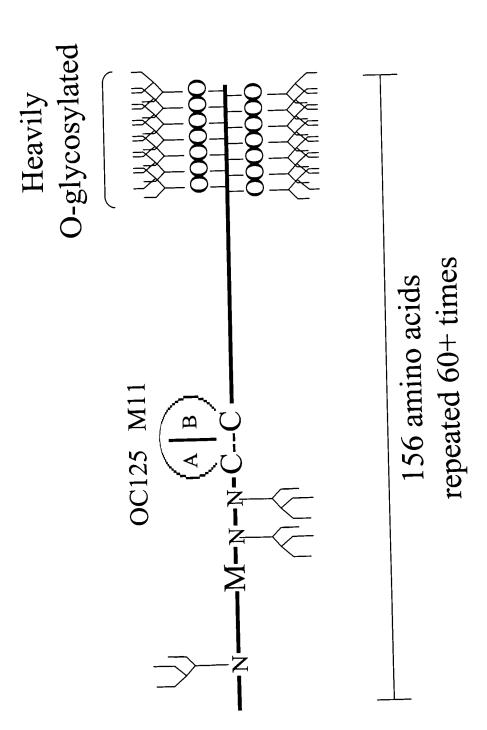


Figure 7A

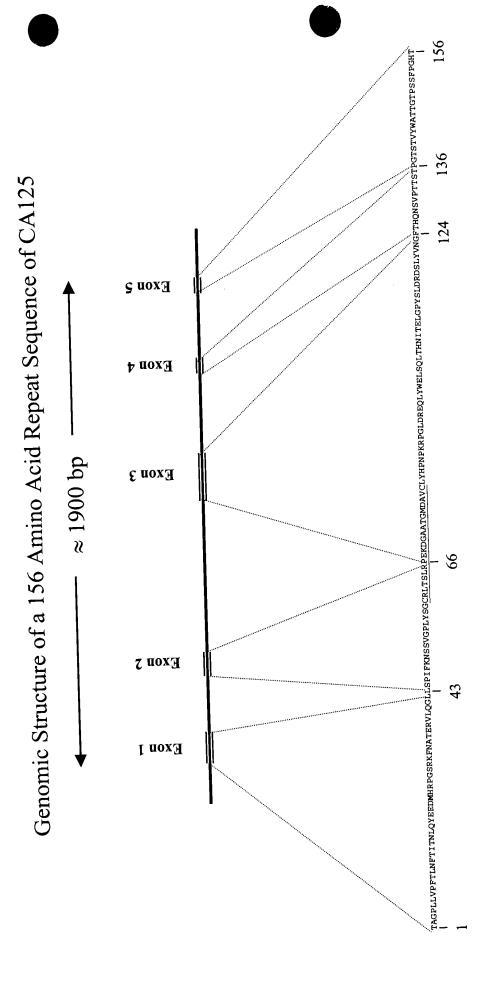


Figure 7B (SEQ ID NO: 163)

## Exon 1

1				
ATVPFMVPFTLNFTITNLQYEEDMRHPGSRKFNATERELQGL (	SEQ	ID 1	10:	164)
TAVPLLVPFTLNFTITNLQYGEDMRHPGSRKFNTTERVLQGL (	SEQ	ID 1	10:	165)
VPGPLLVPFTLNFTITNLQYEEAMRHPGSRKFNTTERVLQGL (	SEQ	ID 1	10:	166)
${\tt APGPLLVPFTLNFTITNLQYEEDMRHPGSRKFSTTERVLQGL} \end{subscription} \begin{subscriptsize} \end{subscriptsize} \beg$	SEQ	ID 1	: 01	167)
APGPLLVPFTLNFTITNLQYEEDMRHPGSRKFNTTERVLQGL (	SEQ	ID 1	: 01	168)
APGPLLVPFTLNFTITNLQYEVDMRHPGSRKFNTTERVLQGL (	SEQ	ID 1	NO:	169)
SAGPLLVPFTLNFTITNLQYEEDMRHPGSRKFNTTERVLQGL (	SEQ	ID 1	: Ои	170)
AAGPLLMPFTLNFTITNLQYEEDMRRTGSRKFNTMESVLQGL (	SEQ	ID I	NO:	171)
TASPLLVLFTINCTITNLQYEEDMRRTGSRKFNTMESVLQGL (	SEQ	ID :	NO:	172)
AAGPLLVPFTLNFTITNLQYGEDMGHPGSRKFNTTERVLQGL (	(SEQ	ID	NO:	173)
TAGPLLIPFTLNFTITNLQYGEDMGHPGSRKFNTTERVLQGL (	(SEQ	ID	NO:	174)
TAGPLLVPFTLNFTITNLQYGEDMGHPGSRKFNTTERVLQGL	(SEQ	ID	NO:	175)
TAGPLLVLFTLNFTITNLKYEEDMHRPGSRKFNTTERVLQTL	(SEQ	ID	NO:	176)
TAGPLLVPFTLNFTITNLQYEEDMHRPGSRKFNATERVLQGL	(SEQ	ID	NO:	177)
TAGPLLVPFTLNFTITNLQYEEDMHRPGSRRFNTTERVLQGL	(SEQ	ID	NO:	178)
TAGPLLVPFTLNFTITNLQYEEDMHRPGSRKFNTTERVLQGL	(SEQ	ID	NO:	179)
APVPLLIPFTLNFTITNLQYEEDMHRPGSRKFNTTERVLQGL	(SEQ	ID	ΝО:	180)
ATGPVLLPFTLNFTITNLQYEEDMHRPGSRKFNTTERVLQGL	(SEQ	ID	NO:	181)
AAGPLLVPFTLNFTITNLQYEEDMHHPGSRKFNTTERVLQGL	(SEQ	ID	NO:	182)
SAGPLLVPFTLNFTITNLQYEEDMHHPGSRKFNTTERVLQGL	(SEQ	ID	NO:	183)
TASPLLVLFTINFTITNQRYEENMHHPGSRKFNTTERVLQGL	(SEQ	ID	NO:	184)
TASPLLVLFTINFTITNLRYEENMHHPGSRKFNTTERVLQGL	(SEQ	] ID	NO:	185)
EPGPLLIPFTFNFTITNLHYEENMQHPGSRKFNTTERVLQGL	(SEQ	] ID	NO:	186)
EPGPLLIPFTFNFTITNLRYEENMQHPGSRKFNTTERVLQGL	(SEÇ	OI O	NO:	187)
APVPLLIPFTLNFTITNLHYEENMQHPGSRKFNTTERVLQGL	(SEÇ	Q ID	NO:	188)
APVPLLIPFTLNFTITDLHYEENMQHPGSRKFNTTERVLQGL	(SEÇ	Q ID	NO:	189)
AASPLLVLFTLNGTITNLRYEENMQHPGSRKFNTTERVLQGL	(SEÇ	Q ID	NO:	190)
TAGPLLVPFTLNFTITNLKYEEDMHCPGSRKFNTTERVLQSL	(SEÇ	) ID	NO:	191)
AASHLLILFTLNFTITNLRYEENMW.PGSRKFNTTERVLQGL	(SEÇ	Q ID	NO:	192)
TGVVSEEPFTLNFTINNLRYMADMGQPGSLKFNITDNVMKHL	(SEC	Q ID	NO:	193)
AMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLL	(SE	Q ID	NO:	194)

### Exon 2

ERUI -	
43 6	
LKPLFRNSSLEYLYSGCRLASI	
LKPLFKNTSVSSLYSGCRLTLL	
LKPLFKNTSVGPLYSGCRLTLI	R (SEQ ID NO: 197)
LKPLFKSTSVGPLYSGCRLTLI	R (SEQ ID NO: 198)
LKPLFKSTSVGPLYSSCRLTLI	R (SEQ ID NO: 199)
LKPLFKNTSVGPLYSGCRLTSI	R (SEQ ID NO: 200)
LGPIFKNTSVGPLYSGCRLTS	LR (SEQ ID NO: 201)
LGPMFKNTSVGLLYSGCRLTL	LR (SEQ ID NO: 202)
LGPMFKNTSVGPLYSGCRLTL	LR (SEQ ID NO: 203)
LGPMFKNTSVGPLYSGCRLTS	LR (SEQ ID NO: 204)
LGPLFKNSSVGPLYSGCRLIS	LR (SEQ ID NO: 205)
LGPLFKNSSVDPLYSGCRLTS	LR (SEQ ID NO: 206)
LSPIFKNSSVGPLYSGCRLTS	LR (SEQ ID NO: 207)
LSPIFKNTSVGPLYSGCRLTL	LR (SEQ ID NO: 208)
LSPLFQRSSLGARYTGCRVIA	LR (SEQ ID NO: 209)
LRPLFKNTSVSSLYSGCRLTL	LR (SEQ ID NO: 210)
LRPLFKNTSVGPLYSGSRLTI	LR (SEQ ID NO: 211)
LRPLFKNTSIGPLYSSCRLTI	LR (SEQ ID NO: 212)
LRPLFKSTSVGPLYSGCRLTI	LR (SEQ ID NO: 213)
LRPVFKNTSVGLLYSGCRLTI	LLR (SEQ ID NO: 214)
LRPVFKNTSVGPLYSGCRLT	LLR (SEQ ID NO: 215)
LRSLFKSTSVGPLYSGCRLT	LLR (SEQ ID NO: 216)
LRSLFKSTSVGPLYSGCRLT	SLR (SEQ ID NO: 217)
LTPLFKNTSVGPLYSGCRLT	LLR (SEQ ID NO: 218)
LTPLFRNTSVSSLYSGCRLT	LLR (SEQ ID NO: 219)
LMPLFKNTSVSSLYSGCRLT	LLR (SEQ ID NO: 220)
RPLFQKSSM.GPFYLGCQLI	SLR (SEQ ID NO: 221)

66

### Exon 3 123

PEKDSSAMAVDAICTHRPDPEDLGLDRERLYWELSNLTNGIQELGPYTLDRNSLYVNG (SEQ ID NO: 222) PEKDGAATGVDAICTHRLDPKSPGLNREQLYWELSKLTNDIEELGPYTLDRNSLYVNG (SEQ ID NO: 223) PKKDGAATGVDAICTHRLDPKSPGLNREQLYWELSKLTNDIEELGPYTLDRNSLYVNG (SEQ ID NO: 224) PEKDGTATGVDAICTHHPDPKSPRLDREQLYWELSQLTHNITELGHYALDNDSLFVNG (SEQ ID NO: 225) PEKDGEATGVDAICTHRPDPTGPGLDREQLYLELSQLTHSITELGPYTLDRDSLYVNG (SEQ ID NO: 226) PEKDGAATGMDAVCLYHPNPKRPGLDREQLYWELSQLTHNITELGPYSLDRDSLYVNG (SEQ ID NO: 227) PEKDGAATGMDAVCLYHPNPKRPGLDREQLYCELSQLTHNITELGPYSLDRDSLYVNG (SEQ ID NO: 228) PEKDGAATRVDAACTYRPDPKSPGLDREQLYWELSQLTHSITELGPYTLDRVSLYVNG (SEQ ID NO: 229) PKKDGAATKVDAICTYRPDPKSPGLDREQLYWELSQLTHSITELGPYTQDRDSLYVNG (SEQ ID NO: 230) PKKDGAATKVDAICTYRPDPKSPGLDREQLYWELSQLTHSITELGPYTQDRDSLYNVG (SEQ ID NO: 231) PEKDGAATRVDAVCTHRPDPKSPGLDRERLYWKLSQLTHGITELGPYTLDRHSLYVNG (SEQ ID NO: 232) PEKDGVATRVDAICTHRPDPKIPGLDRQQLYWELSQLTHSITELGPYTLDRDSLYVNG (SEQ ID NO: 233) SEKDGAATGVDAICIHHLDPKSPGLNRERLYWELSQLTNGIKELGPYTLDRNSLYVNG (SEQ ID NO: 234) SEKDGAATGVDAICTHRLDPKSPGLDREQLYWELSQLTNGIKELGPYTLDRNSLYVNG (SEQ ID NO: 235) SEKDGAATGVDAICTHRLDPKSPGVDREQLYWELSQLTNGIKELGPYTLDRNSLYVNG (SEQ ID NO: 236) SEKDGAATGVDAICTHRVDPKSPGVDREQLYWELSQLTNGIKELGPYTLDRNSLYVNG (SEQ ID NO: 237) SEKDGAATGVDAICTHHLNPQSPGLDREQLYWQLSQMTNGIKELGPYTLDRNSLYVNG (SEQ ID NO: 238) PEKRGAATGVDTICTHRLDPLNPGLDREQLYWELSKLTRGIIELGPYLLDRGSLYVNG (SEQ ID NO: 239) PEKNGAATGMDAICSHRLDPKSPGLNREQLYWELSQLTHGIKELGPYTLDRNSLYVNG (SEQ ID NO: 240) PEKNGAATGMDAICSHRLDPKSPGLDREQLYWELSQLTHGIKELGPYTLDRNSLYVNG (SEQ ID NO: 241) PEKHGAATGVDAICTLRLDPTGPGLDRERLYWELSQLTNSVTELGPYTLDRDSLYVNG (SEQ ID NO: 242) PEKHGAATGVDAICTLRLDPTGPGLDRERLYWELSQLTNSITELGPYTLDRDSLYVNG (SEQ ID NO: 243) PEKHEAATGVDTICTHRVDPIGPGLDRERLYWELSQLTNSITELGPYTLDRDSLYVNG (SEQ ID NO: 244) PEKQEAATGVDTICTHRVDPIGPGLDRERLYWELSQLTNSITELGPYTLDRDSLYVNG (SEQ ID NO: 245) PEKQEAATGVDTICTHRVDPIGPGLDRERLYWELSQLTNSITELGPYTLDRDSLYVDG (SEQ ID NO: 246) PEKDKAATRVDAICTHHPDPQSPGLNREQLYWELSQLTHGITELGPYTLDRDSLYVDG (SEQ ID NO: 247) SVKNGAETRVDLLCTYLQPLSGPGLPIKQVFHELSQQTHGITRLGPYSLDKDSLYLNG (SEQ ID NO: 248) PEKDGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTHGVTQLGFYVLDRDSLFING (SEQ ID NO: 249)

### Exon 4

124 135 FTHRSSMPTTST (SEQ ID NO: 250) FTHRSSMPTTSI (SEQ ID NO: 251) FTHRTSVPTSST (SEQ ID NO: 252) FTHRTSVPTTST (SEQ ID NO: 253) FTHRSSVPTTSS (SEQ ID NO: 254) FTHRSSVSTTST (SEQ ID NO: 255) FTHRSSVAPTST (SEQ ID NO: 256) FTHRSSGLTTST (SEQ ID NO: 257) FTHRSFGLTTST (SEQ ID NO: 258) FTHRSSFLTTST (SEQ ID NO: 259) FTHRNFVPITST (SEQ ID NO: 260)

FTHRSSVPTTSI (SEQ ID NO: 261)

FTHQSSVSTTST (SEQ ID NO: 262) FTHQTSAPNTST (SEQ ID NO: 263) FTHQTFAPNTST (SEQ ID NO: 264)

FTHQNSVPTTST (SEQ ID NO: 265) FTHQSSMTTTRT (SEQ ID NO: 266) FTHWIPVPTSST (SEQ ID NO: 267)

FTHWSPIPTTST (SEQ ID NO: 268) FTHWSSGLTTST (SEQ ID NO: 269)

FHPRSSVPTTST (SEQ ID NO: 270) FNPRSSVPTTST (SEQ ID NO: 271)

FNPWSSVPTTST (SEQ ID NO: 272) FTQRSSVPTTSI (SEQ ID NO: 273)

FTQRSSVPTTST (SEQ ID NO: 274)

FTQRSSVPTTSV (SEQ ID NO: 275) YNEPGLDEPPTT (SEQ ID NO: 276)

YAPQNLSIRGEY (SEQ ID NO: 277)

### Exon 5

156 136

PGTSTVDVGTSGTPSSSPSPT PGTSTVDLRTSGTPSSLSSPTIM PGTSTVDLGTSGTPFSLPSPA PGTSTVDLG.SGTPSSLPSPT PGTSTVDLG.SGTPSLPSSPT PGTSTVDLGTSGTPSSLPSPT PGTPTVDLGTSGTPVSKPGPS PWTSTVDLGTSGTPSPVPSPT PGTSTVYWATTGTPSSFPGHT PGTSTVHLATSGTPSSLPGHT PGTSTVHLATSGTPSPLPGHT PDTSTMHLATSRTPASLSGPT PGTSAVHLETSGTPASLPGHT PGTSAVHLETTGTPSSFPGHT

PGTSTVHLGTSETPSSLPRPI PGTSIVNLGTSGIPPSLPETT PGTFTVQPETSETPSSLPGPT

PGTPTVDLGTSGTPVSKPGPS PGTPTVYLGASKTPASIFGPS

PKPATTFLPPLSEATT.... QINFHIVNWNLSNPDPTSSEY (SEQ ID NO: 278) (SEQ ID NO: 279) (SEQ ID NO: 280) (SEQ ID NO: 281) (SEQ ID NO: 282) (SEQ ID NO: 283) (SEQ ID NO: 284)

(SEQ ID NO: 285) (SEQ ID NO: 286) (SEQ ID NO: 287) (SEQ ID NO: 288) (SEQ ID NO: 289) (SEQ ID NO: 290)

(SEQ ID NO: 291) (SEQ ID NO: 292) (SEQ ID NO: 293) (SEQ ID NO: 294)

(SEQ ID NO: 295) (SEQ ID NO: 296) (SEQ ID NO: 297) (SEQ ID NO: 298)

Structure of Amino Terminal Domain

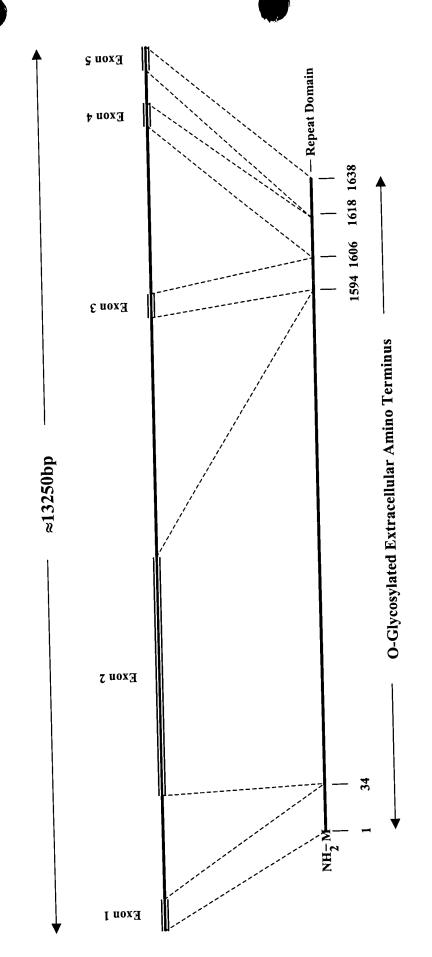


Figure 8A

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SQPETIDSWV AHPGTEASSV VPTLTVSTGE PFTNISLVTH PAESSSTLPR TTSRFSHSEL DIMPSTVTSP EAESSSAIST TISPGIPGVL TSLVTSSGRD O TESLVTHSEA KMISAIPTLA VSPTVQGLVT SLVTSSGSET SAFSNLTVAS SASSAVPTPT VSPGVSGVVT PLVTSSRAVT STTIPILTLS SSEPETTPSM ATSHGVEASS AVLTVSPEVP GMVTSLVTSS RAVTSTTIPT LTISSDEPET VLPEVPGMVT SLVASSRAVT STTLPTLTLS PGEPETTPSM ATSHGAEASS TVPTVSPEVP GVVTSLVTSS SGVNSTSIPT LILSPGELET TPSMATSHGA VPGVVTSLVT SSRAVTSTTI PILTFSLGEP ETTPSMATSH GTEAGSAVPT PLVTSSRAVI STTIPILTLS PGEPETTPSM ATSHGEEASS AIPTPTVSPG SPGAEDLVTS QVTSSGTDRN MTIPTLTLSP GEPKTIASLV THPEAQTSSA OOO OOO SELVISMVIS LAAKTSTINR ALINSPGEPA TIVSLVIHPA RITWLTHPAE TSSTIPRTIP NFSHHESDAT PSIATSPGAE TSSAIPIMTV SHGADVSSA IPTNISPSEL DALTPLVTIS GTDTSTTFPT LTKSPHETET MEHITKIPNE AAHRGTIRPV KGPQTSTSPA SPKGLHTGGT KRMETTTTAL SOSO STATIALKIT SRATLITSVY TPILGTLIPL NASROMASTI LIEMMITTPY VPPDVPETTS SLATSLGAET STALPRITIPS VLNRESETTA SLVSRSGAER SPVIQTLDVS SSEPDTTASW VIHPAETIPT VSKTTPNFFH SELDTVSSTA

801

601

501

401

301

201

STISSYNRR YWTPAISTPV ISTFSPGIST SSIPSSTAAT VPFMVPFTLN FIIINLQYEE DMRHPGSRKF NATERELQGL LKPLFRNSSL EYLYSG $\overline{\mathrm{CRLA}}$ PSSSAETSTS TLTLTVSPAV SGLSSASITT DKPQTVTSWN TETSPSVTSV GPPEFSRTVT GTTMTLIPSE MPTPPKTSHG EGVSPTTILR TTMVEATNLA PRGSSPTVAK TITTENTLAG SLFTPLTTPG MSTLASESVT SRTSYNHRSW TSRVDLSPTA SPGVSAKTAP LSTHPGTETS TMIPTSTLSL GLLETTGLLA HPAETSTIVS GIIPNESHRG SDIAPSMVIS PGVDTRSGVP TITIPPSIPG WASQVISSA IDISTAIPIL IPSPGEPETT ASSATHPGTQ TGFTVPIRTV PSSEPDTMAS WVTHPPQTST PVSRTTSSFS HSSPDATPVM ATSPRTEASS AVLTTISPGA PEMVTSQITS SGAATSTTVP TLTHSPGMPE TTALLSTHPR PETSKIFPAS TVFPQVSETT ASLTIRPGAE TSTALPTQTT SSLFTLLVTG ETTTSFITYS ETHTSSAIPT LPVSPGASKM LTSLVISSGT DSTTTFPTLT ETPYEPETTA IQLIHPAETN TMVPRTTPKF SHSKSDTTLP VAITSPGPEA ISATEPTVPE SPHESEATAS WVTHPAVTST TVPRTTPNYS HSEPDTTPSI ATSPGAEATS DFPTITVSPD VPDMVTSQVT SSGTDTSITI PTLTLSSGEP SLRPEKDSSA MAVDAICTHR PDPEDLGLDR ERLYWELSÑL TNGIQEY SSAVSTTTIS PDMSDLVTSL VPSSGTDTST TFPTLSETPY EPETTAL TLDRNSLYVN GFTHRSSMPT TSTPGTSTVD VGTSGTPSSS PSPT 1651 1751 1601 1301 1351 1401 1501 1201 1451 1251 1551 1151 1101 1001 1051

TELECE SELECE
Stucture of Carboxy Terminal Domain

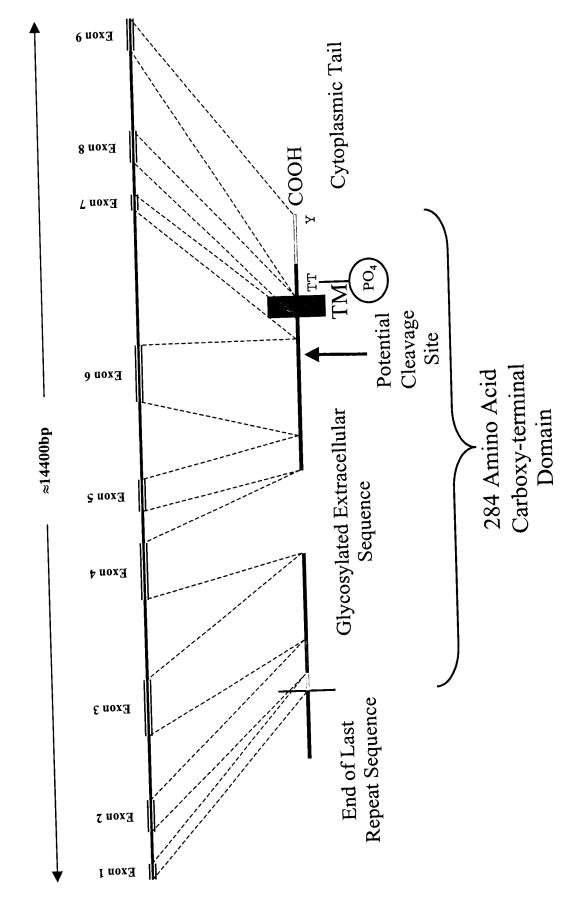
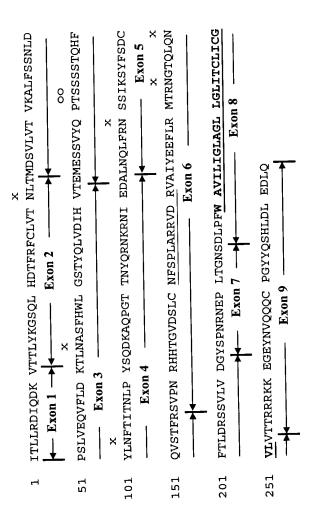


Figure 9A



# Proposed Structure of CA125

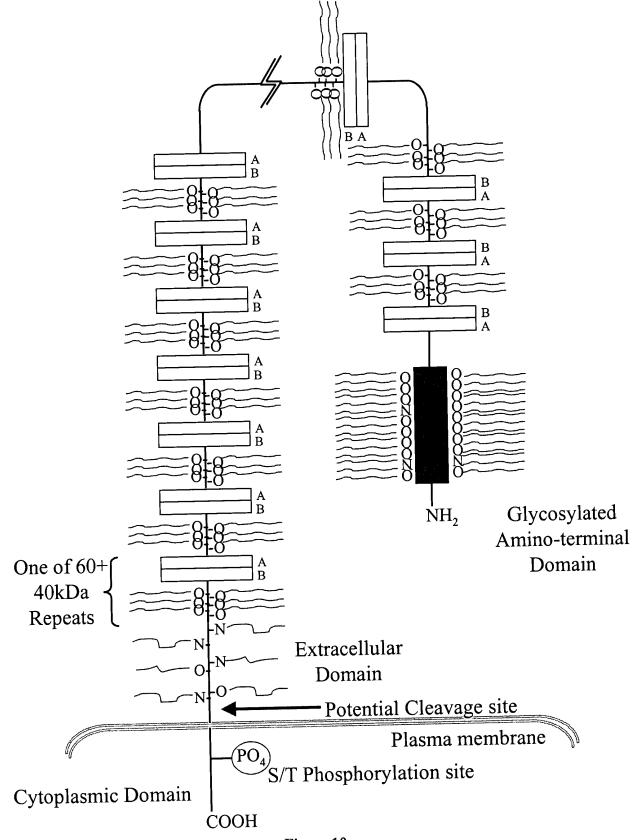


Figure 10